

SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT, K⁺-betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE

<130> D0121 NP

<150> US 60/270,132

<151> 2001-02-21

<150> US 60/278,953

<151> 2001-03-27

<160> 74

<170> PatentIn version 3.0

<210> 1

<211> 2052

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (121)..(1095)

<400> 1

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atg gct ctg gcg gac aca cgt gga tta ccc aac ggg ggc ggc ggc 168
Met Ala Leu Ala Asp Ser Thr Arg Gly Leu Pro Asn Gly Gly Gly Gly
1 5 10 15ggg ggc ggc agt ggc tcc tcg tcc tcc gcg gag cca ccg ctc ttc 216
Gly Gly Ser Gly Ser Ser Ser Ala Glu Pro Pro Leu Phe
20 25 30ccc gac atc gtg gag ctg aac gtg ggg ggc cag gtg tac gtg acc cgg 264
Pro Asp Ile Val Glu Leu Asn Val Gly Gly Gln Val Tyr Val Thr Arg
35 40 45cgc tgc acg gtg gtg tcg ccc gac tcg ctg ctc tgg cgc atg ttc 312
Arg Cys Thr Val Val Ser Val Pro Asp Ser Leu Leu Trp Arg Met Phe
50 55 60acg cag cag cag ccg cag gag ctg gcc cgg gac agc aaa ggc cgc ttc 360
Thr Gln Gln Pro Gln Glu Leu Ala Arg Asp Ser Lys Gly Arg Phe
65 70 75 80ttt ctg gac cgg gac ggc ttc ctc ttc cgc tac atc ctg gat tac ctg 408
Phe Leu Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu
85 90 95

ccg gac ttg cag ctc gtg ctc ccc gac tac ttc ccc gag cgc agc cgg	456
Arg Asp Leu Gln Leu Val Leu Pro Asp Tyr Phe Pro Glu Arg Ser Arg	
100 105 110	
ctg cag ccc gag gcc gag tac ttc gag ctg cca gag ctc gtg cgc cgg	504
Leu Gln Arg Glu Ala Glu Tyr Phe Glu Leu Pro Glu Leu Val Arg Arg	
115 120 125	
ctc ggg gcg ccc cag cag ccc ggc ccc ggg cgg ccc tcg cgg cgg	552
Leu Gly Ala Pro Gln Gln Pro Gly Pro Gly Pro Pro Ser Arg Arg	
130 135 140	
ggg gtg cac aag gag ggc tcg ggt gac gag ctg ctg ccc ctt ggc	600
Gly Val His Lys Glu Gly Ser Leu Gly Asp Glu Leu Leu Pro Leu Gly	
145 150 155 160	
tac tcg gag ccc gaa cag cag gag ggc gcc tct gcc ggg gcg ccc tcg	648
Tyr Ser Glu Pro Glu Gln Glu Gly Ala Ser Ala Gly Ala Pro Ser	
165 170 175	
ccc acg ctg gag ctg gct agc cgc agt ccc tcc ggg ggc gcg gcg	696
Pro Thr Leu Glu Leu Ala Ser Arg Ser Pro Ser Gly Gly Ala Ala Gly	
180 185 190	
ccg ctg ctc acg ccc tcc cag tcg ctg gac ggc agc cgg cgc tcg ggc	744
Pro Leu Leu Thr Pro Ser Gln Ser Leu Asp Gly Ser Arg Arg Ser Gly	
195 200 205	
tac atc acc atc ggc tac cgc ggc tcc tac acc atc ggg cgg gac gcg	792
Tyr Ile Thr Ile Gly Tyr Arg Gly Ser Tyr Thr Ile Gly Arg Asp Ala	
210 215 220	
cag gcg gac gcc aag ttc cgg cga gtg gcg cgc atc acc gtt tgc gga	840
Gln Ala Asp Ala Lys Phe Arg Arg Val Ala Arg Ile Thr Val Cys Gly	
225 230 235 240	
aag acg tcg ctg gcc aag gag gtg ttt ggg gac acc ctg aac gaa agc	888
Lys Thr Ser Leu Ala Lys Glu Val Phe Gly Asp Thr Leu Asn Glu Ser	
245 250 255	
ccg gac ccc gac cgt ccc ccc gag cgc tac acc tcg cgc tat tac ctc	936
Arg Asp Pro Asp Arg Pro Pro Glu Arg Tyr Thr Ser Arg Tyr Tyr Leu	
260 265 270	
aag ttc aac ttc ctg gag cag gcc ttc gac aag ctg tcc gag tcg ggc	984
Lys Phe Asn Phe Leu Glu Gln Ala Phe Asp Lys Leu Ser Glu Ser Gly	
275 280 285	
ttc cac atg gtg gcg tgc agc tcc acg ggc acc tgc gcc ttt gcc agc	1032
Phe His Met Val Ala Cys Ser Ser Thr Gly Thr Cys Ala Phe Ala Ser	
290 295 300	
agc acc gac cag agc gag gac aag atc tgg acc agc tac acc gag tac	1080
Ser Thr Asp Gln Ser Glu Asp Lys Ile Trp Thr Ser Tyr Thr Glu Tyr	
305 310 315 320	
gtc ttc tgc agg gag tgagctcccc agaccccccgcactccag cggccaggccc	1135

Val Phe Cys Arg Glu
325

ttctctgtcc	cgagagatga	ttacagagcc	tcttgcucca	cctttgtccc	ctgggtgtcg	1195
ccatccatt	ctccccctcc	agtagtagct	gggtgagacc	tgtccgcucca	ccttccctcc	1255
actacagaac	ctggcagccgc	aaatccctcg	ggctgcttcg	tcttctttgg	acccctgtaa	1315
ccgagagaac	ccagaggaac	ccccacccca	cccccaccta	ccactccatg	ctttctctac	1375
tccctgcctc	aaaccacccc	tccccagat	ggtacttcag	tttggatcta	ttgggggagt	1435
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cccatggagg	cagtcctcaa	accacccctc	ccccagatgg	tacttcagtt	tggatctatt	1735
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aagagatcg	gattggttcc	actgtctggg	gttagtgttt	tacaaggtca	ttacacagtc	1915
tttttgacct	cttttgaagg	tagagttta	gaaggctgga	tggaagattc	tgagcctgga	1975
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<211> 325
<212> PRT
<213> homo sapiens

<400> 2

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Gly Gly Gly Ser Gly Ser Ser Ser Ser Ala Glu Pro Pro Leu Phe
20 25 30

Pro Asp Ile Val Glu Leu Asn Val Gly Gly Gln Val Tyr Val Thr Arg
35 40 45

Arg Cys Thr Val Val Ser Val Pro Asp Ser Leu Leu Trp Arg Met Phe
50 55 60

Thr Gln Gln Gln Pro Gln Glu Leu Ala Arg Asp Ser Lys Gly Arg Phe
65 70 75 80

Phe Leu Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu
85 90 95

Arg Asp Leu Gln Leu Val Leu Pro Asp Tyr Phe Pro Glu Arg Ser Arg
100 105 110

Leu Gln Arg Glu Ala Glu Tyr Phe Glu Leu Pro Glu Leu Val Arg Arg
115 120 125

Leu Gly Ala Pro Gln Gln Pro Gly Pro Gly Pro Pro Ser Arg Arg
130 135 140

Gly Val His Lys Glu Gly Ser Leu Gly Asp Glu Leu Leu Pro Leu Gly
145 150 155 160

Tyr Ser Glu Pro Glu Gln Glu Gly Ala Ser Ala Gly Ala Pro Ser
165 170 175

Pro Thr Leu Glu Leu Ala Ser Arg Ser Pro Ser Gly Gly Ala Ala Gly
180 185 190

Pro Leu Leu Thr Pro Ser Gln Ser Leu Asp Gly Ser Arg Arg Ser Gly
195 200 205

Tyr Ile Thr Ile Gly Tyr Arg Gly Ser Tyr Thr Ile Gly Arg Asp Ala
210 215 220

Gln Ala Asp Ala Lys Phe Arg Arg Val Ala Arg Ile Thr Val Cys Gly
225 230 235 240

Lys Thr Ser Leu Ala Lys Glu Val Phe Gly Asp Thr Leu Asn Glu Ser
245 250 255

Arg Asp Pro Asp Arg Prc Pro Glu Arg Tyr Thr Ser Arg Tyr Tyr Leu
260 265 270

Lys Phe Asn Phe Leu Glu Gln Ala Phe Asp Lys Leu Ser Glu Ser Gly
275 280 285

Phe His Met Val Ala Cys Ser Ser Thr Gly Thr Cys Ala Phe Ala Ser
290 295 300

Ser Thr Asp Gln Ser Glu Asp Lys Ile Trp Thr Ser Tyr Thr Glu Tyr
305 310 315 320

Val Phe Cys Arg Glu
325

<210> 3
<211> 228
<212> PRT
<213> Drosophila melanogaster

<400> 3

Met Pro Glu Ile Ile Glu Leu Asn Val Gly Gly Val Ser Tyr Thr Thr
1 5 10 15

Thr Leu Ala Thr Leu Leu Gln Asp Lys Ser Thr Leu Leu Ala Glu Leu
20 25 30

Phe Gly Glu Gly Arg Asp Ser Leu Ala Lys Asp Ser Lys Gly Arg Tyr
35 40 45

Phe Leu Asp Arg Asp Gly Val Leu Phe Arg Tyr Ile Leu Asp Phe Leu
50 55 60

Arg Asp Lys Ala Leu His Leu Pro Glu Gly Phe Arg Glu Arg Gln Arg
65 70 75 80

Leu Leu Arg Glu Ala Glu His Phe Lys Leu Thr Ala Met Leu Glu Cys
85 90 95

Ile Arg Ser Glu Arg Asp Ala Arg Pro Pro Gly Cys Ile Thr Ile Gly
100 105 110

Tyr Arg Gly Ser Phe Gln Phe Gly Lys Asp Gly Leu Ala Asp Val Lys
115 120 125

Phe Arg Lys Leu Ser Arg Ile Leu Val Cys Gly Arg Val Ala Gln Cys
130 135 140

Arg Glu Val Phe Gly Asp Thr Leu Asn Glu Ser Arg Asp Pro Asp His
145 150 155 160

Gly Gly Thr Asp Arg Tyr Thr Ser Arg Phe Phe Leu Lys His Cys Tyr
165 170 175

Ile Glu Gln Ala Phe Asp Asn Leu His Asp His Gly Tyr Arg Met Ala
180 185 190

Gly Ser Cys Gly Ser Gly Thr Ala Gly Ser Ala Ala Glu Pro Lys Pro

195

200

205

Gly Val Asp Thr Glu Glu Asn Arg Trp Asn His Tyr Asn Glu Phe Val
210 215 220

Phe Ile Arg Asp
225

<210> 4
<211> 435
<212> PRT
<213> Homo sapiens

<400> 4

Gln Gln Gln Lys Lys Gly Thr Met Ala Leu Ser Gly Asn Cys Ser Arg
1 5 10 15

Tyr Tyr Pro Arg Glu Gln Gly Ser Ala Val Pro Asn Ser Phe Pro Glu
20 25 30

Val Val Glu Leu Asn Val Gly Gly Gln Val Tyr Phe Thr Arg His Ser
35 40 45

Thr Leu Ile Ser Ile Pro His Ser Leu Leu Trp Lys Met Phe Ser Pro
50 55 60

Lys Arg Asp Thr Ala Asn Asp Leu Ala Lys Asp Ser Lys Gly Arg Phe
65 70 75 80

Phe Ile Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu
85 90 95

Arg Asp Arg Gln Val Val Leu Pro Asp His Phe Pro Glu Lys Gly Arg
100 105 110

Leu Lys Arg Glu Ala Glu Tyr Phe Gln Leu Pro Asp Leu Val Lys Leu
115 120 125

Leu Thr Pro Asp Glu Ile Lys Gln Ser Pro Asp Glu Phe Cys His Ser
130 135 140

Asp Phe Glu Asp Ala Ser Gln Gly Ser Asp Thr Arg Ile Cys Pro Pro
145 150 155 160

Ser Ser Leu Leu Pro Ala Asp Arg Lys Trp Gly Phe Ile Thr Val Gly
165 170 175

Tyr Arg Gly Ser Cys Thr Leu Gly Arg Glu Gly Gln Ala Asp Ala Lys
180 185 190

Phe Arg Arg Val Pro Arg Ile Leu Val Cys Gly Arg Ile Ser Leu Ala
195 200 205

Lys Glu Val Phe Gly Glu Thr Leu Asn Glu Ser Arg Asp Pro Asp Arg
210 215 220

Ala Pro Glu Arg Tyr Thr Ser Arg Phe Tyr Leu Lys Phe Lys His Leu
225 230 235 240

Glu Arg Ala Phe Asp Met Leu Ser Glu Cys Gly Phe His Met Val Ala
245 250 255

Cys Asn Ser Ser Val Thr Ala Ser Phe Ile Asn Gln Tyr Thr Asp Asp
260 265 270

Lys Ile Trp Ser Ser Tyr Thr Glu Tyr Val Phe Tyr Arg Glu Pro Ser
275 280 285

Arg Trp Ser Pro Ser His Cys Asp Cys Cys Cys Lys Asn Gly Lys Gly
290 295 300

Asp Lys Glu Gly Glu Ser Gly Thr Ser Cys Asn Asp Leu Ser Thr Ser
305 310 315 320

Ser Cys Asp Ser Gln Ser Glu Ala Ser Ser Pro Gln Glu Thr Val Ile
325 330 335

Cys Gly Pro Val Thr Arg Gln Thr Asn Ile Gln Thr Leu Asp Arg Pro
340 345 350

Ile Lys Lys Gly Pro Val Gln Leu Ile Gln Gln Ser Glu Met Arg Arg
355 360 365

Lys Ser Asp Leu Leu Arg Thr Leu Thr Ser Gly Ser Arg Glu Ser Asn
370 375 380

Met Ser Ser Lys Lys Ala Val Lys Glu Lys Leu Ser Ile Glu Glu
385 390 395 400

Glu Leu Glu Lys Cys Ile Gln Asp Phe Leu Lys Ile Lys Ile Pro Asp
405 410 415

Arg Phe Pro Glu Arg Lys His Pro Trp Gln Ser Glu Leu Leu Arg Lys
420 425 430

Tyr His Leu
435

<110> 5
<211> 140
<212> PRT
<213> *Caenorhabditis elegans*

<400> 5

Met Thr Ser Val Glu Asp Val Ile Thr Leu Asn Val Gly Gly Thr Met
1 5 10 15

Tyr Thr Thr Arg Ser Thr Leu Ser Lys Glu Thr Asp Thr Leu Leu
20 25 30

Ala Asn Ile Ala Ser Gly Ser Leu Ser Glu Asp Glu Gln Ala Asn Val
35 40 45

Val Thr Leu Pro Asp Gly Thr Leu Phe Val Asp Arg Asp Gly Pro Leu
50 55 60

Phe Ala Tyr Val Leu His Phe Leu Arg Thr Asp Lys Leu Ser Leu Pro
65 70 75 80

Glu Gln Phe Arg Glu Val Ala Arg Leu Lys Asp Glu Ala Asp Phe Tyr
85 90 95

Arg Leu Glu Arg Phe Ser Thr Leu Leu Ser Asn Ala Ser Ser Ile Ser
100 105 110

Pro Arg Pro Arg Thr Ala Asn Gly Tyr Asn Thr Ile Thr Ser Gly Ala
115 120 125

Glu Thr Gly Gly Tyr Ile Thr Leu Gly Tyr Arg Gly
130 135 140

<210> 6

<211> 256

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (15)...(15)

<223> wherein "X" is equal to any amino acid.

<400> 6

Met Ser Arg Pro Leu Ile Thr Arg Ser Pro Ala Ser Pro Leu Xaa Asn
1 5 10 15

Gln Gly Ile Pro Thr Pro Ala Gln Leu Thr Lys Ser Asn Ala Pro Val
20 25 30

His Ile Asp Val Gly Gly His Met Tyr Thr Ser Ser Leu Ala Thr Leu
35 40 45

Thr Lys Tyr Pro Glu Ser Arg Ile Gly Arg Leu Phe Asp Gly Thr Glu
50 55 60

Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp
65 70 75 80

Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu
85 90 95

Leu Ile Pro Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala
100 105 110

Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys
115 120 125

Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val

130

135

140

Val Arg Val Ala Pro Asp Leu Gly Glu Arg Ile Thr Leu Ser Gly Asp
145 150 155 160

Lys Ser Leu Ile Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys
165 170 175

Asn Ser Val Asn Ala Gly Trp Asn His Asp Ser Thr His Val Ile Arg
180 185 190

Phe Pro Leu Asn Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu
195 200 205

Arg Leu Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Gly Gly
210 215 220

Val Asp Ser Ser Gln Phe Ser Glu Tyr Val Leu Arg Arg Glu Leu Arg
225 230 235 240

Arg Thr Pro Arg Val Pro Ser Val Ile Arg Ile Lys Gln Glu Pro Leu
245 250 255

<210> 7

<211> 237

<212> PRT

<213> Homo sapiens

<400> 7

Met Asp Asn Gly Asp Trp Gly Tyr Met Met Thr Asp Pro Val Thr Leu
1 5 10 15

Asn Val Gly Gly His Leu Tyr Thr Thr Ser Leu Thr Thr Leu Thr Arg
20 25 30

Tyr Pro Asp Ser Met Leu Gly Ala Met Phe Gly Asp Phe Pro Thr
35 40 45

Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu
50 55 60

Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro
65 70 75 80

Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr
85 90 95

Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr
100 105 110

Pro Met Asp Thr Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys
115 120 125

Leu Ser Lys Tyr Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr
130 135 140

Ile Thr Thr Lys Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe
145 150 155 160

Thr Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser
165 170 175

Phe Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val
180 185 190

His Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr
195 200 205

Arg Val His His Met Ser Glu Arg Ala Asn Glu Asn Thr Val Glu His
210 215 220

Asn Trp Thr Phe Cys Arg Leu Ala Arg Lys Thr Asp Asp
225 230 235

<210> 8
<211> 688
<212> DNA
<213> homo sapiens

<220>
<221> misc_feature
<223> wherein "N" is equal to "A", "C", "G" or "T".

<400> 8
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gagtgcagcg cggcttcctg ccactgtccc ggcccgccca cctctctgtc atggctctgg 120
cgAACAGCAC acgtggatta cccaannnnn nnnnnnnnnn nnnnnnnnagt ggctcctcgt 180
cgtcctccgc ggagccaccc ctcttccccg acatcgtgga gctgaacgtg gggggccagg 240
tgtacgtgac cccgcgtgc acggtggtgt cggtgcccga ctcgctgctc tggcgcatgt 300
tcacgcagca gcagccgcag gagctggccc gggacagcaa aggccgcttc tttctggacc 360
gggacggctt cctcttcgc tacatcctgg attacctgcg ggacttgcag ctcgtgctgc 420
ccgactactt ccccgagcgc agccggctgc agcgcgaggc cgagtacttc gagctgccag 480
agctcgtnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 540
nnnnnnntgca caaggagggc tcgctgggtg acgagctgct gccgcttggc tactcggago 600
ccgaacagca ggagggcgcc tctgccgggg cgccgtcgcc cacgctggag ctggctagcc 660
gcagtccgtt nnnnnnnnnn nnnnnnnn 688

<210> 9
<211> 237
<212> PRT

<213> homo sapiens

<400> 9

Met Asp Asn Gly Asp Trp Gly Tyr Met Met Thr Asp Pro Val Thr Leu
1 5 10 15

Asn Val Gly Gly His Leu Tyr Thr Thr Ser Leu Thr Thr Leu Thr Arg
20 25 30

Tyr Pro Asp Ser Met Leu Gly Ala Met Phe Gly Gly Asp Phe Pro Thr
35 40 45

Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu
50 55 60

Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro
65 70 75 80

Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr
85 90 95

Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr
100 105 110

Pro Met Asp Thr Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys
115 120 125

Leu Ser Lys Tyr Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr
130 135 140

Ile Thr Thr Lys Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe
145 150 155 160

Thr Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser
165 170 175

Phe Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val
180 185 190

His Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr
195 200 205

Arg Val His His Met Ser Glu Arg Ala Asn Glu Asn Thr Val Glu His
210 215 220

Asn Trp Thr Phe Cys Arg Leu Ala Arg Lys Thr Asp Asp
225 230 235

<210> 10

<211> 80

<212> DNA

<213> homo sapiens

<400> 10

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aggatgtac ggaagaggaa

50

<210> 11
<211> 19
<212> DNA
<213> homo sapiens

<400> 11
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19

<210> 12
<211> 20
<212> DNA
<213> homo sapiens

<400> 12
agctctggca gctcgaagta

20

<210> 13
<211> 101
<212> PRT
<213> homo sapiens

<400> 13

Asp Ile Val Glu Leu Asn Val Gly Gly Gln Val Tyr Val Thr Arg Arg
1 5 10 15

Cys Thr Val Val Ser Val Pro Asp Ser Leu Leu Trp Arg Met Phe Thr
20 25 30

Gln Gln Gln Pro Gln Glu Leu Ala Arg Asp Ser Lys Gly Arg Phe Phe
35 40 45

Leu Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu Arg
50 55 60

Asp Leu Gln Leu Val Leu Pro Asp Tyr Phe Pro Glu Arg Ser Arg Leu
65 70 75 80

Gln Arg Glu Ala Glu Tyr Phe Glu Leu Pro Glu Leu Val Arg Arg Leu
85 90 95

Gly Ala Pro Gln Gln
100

<210> 14
<211> 13
<212> PRT
<213> homo sapiens

<400> 14

Met Ala Leu Ala Asp Ser Thr Arg Gly Leu Pro Asn Gly

1

5

10

<210> 15
<211> 13
<212> PRT
<213> homo sapiens

<400> 15

Gly Gln Val Tyr Val Thr Arg Arg Cys Thr Val Val Ser
1 5 10

<210> 16
<211> 13
<212> PRT
<213> homo sapiens

<400> 16

Pro Gly Pro Pro Pro Ser Arg Arg Gly Val His Lys Glu
1 5 10

<210> 17
<211> 13
<212> PRT
<213> homo sapiens

<400> 17

Gln Ser Leu Asp Gly Ser Arg Arg Ser Gly Tyr Ile Thr
1 5 10

<210> 18
<211> 13
<212> PRT
<213> homo sapiens

<400> 18

Pro Pro Glu Arg Tyr Thr Ser Arg Tyr Tyr Leu Lys Phe
1 5 10

<210> 19
<211> 18
<212> PRT
<213> homo sapiens

<400> 19

Phe Pro Glu Arg Ser Arg Leu Gln Arg Glu Ala Glu Tyr Phe Glu Leu
1 5 10 15

Pro Glu

<210> 20
<211> 14

<211> PRT
<213> homo sapiens

<400> 20

Phe Gly Asp Thr Leu Asn Glu Ser Arg Asp Pro Asp Arg Pro
1 5 10

<210> 21
<211> 20
<212> PRT
<213> homo sapiens

<400> 21

Leu Ser Glu Ser Gly Phe His Met Val Ala Cys Ser Ser Thr Gly Thr
1 5 10 15

Cys Ala Phe Ala
20

<210> 12
<211> 8
<212> PRT
<213> bacteriophage T7

<400> 12

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 23
<211> 733
<212> DNA
<213> homo sapiens

<400> 23

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tctcccgac	tcctgaggtc	acatgcgtgg	tggtggacgt	aagccacgaa	gaccctgagg	180
tcaagttcaa	ctggtagtgc	gacggcgtgg	aggtgcataa	tgccaagaca	aagccgcggg	240
aggagcagta	caacagcacg	taccgtgtgg	tcagcgtcct	caccgtcctg	caccaggact	300
ggctgaatgg	caaggagtagc	aagtgcagg	tctccaacaa	agccctccca	accccccatacg	360
agaaaaccat	ctccaaagcc	aaagggcago	cccgagaacc	acaggtgtac	accctgcccc	420
catcccgaaa	tgagctgacc	aagaaccagg	tcagcctgac	ctgcctggtc	aaaggcttct	480
atccaaggcga	catcgccgtg	gagtgggaga	gcaatggca	gccggagaac	aactacaaga	540
ccacgcctcc	cgtgcgtggac	cccgacggct	ccttcttcct	ctacagcaag	ctcacccgtgg	600

aca a gagg ag g t ggc a g ag g g gaacgt ct tctcat g tc c g tgat g at gag g ct ct gc	660
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gact ct ag ag gat	733
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<213> Homo sapiens	
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<212> DNA	
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<213> Homo sapiens	
<400> 26	
gc a g c ag cg g c c gcat gg ct ct g gg c g a ca gc a ca c gt g	39
<210> 27	
<211> 37	
<212> DNA	
<213> Homo sapiens	
<400> 27	
gc a g c ag cg g ac c ttgt c ga agg c t g tc c a ggaag	37
<210> 28	
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<400> 28	
cagg t gc a cc t g gtgc a gt c t g g	23
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<211> 23	
<212> DNA	
<213> Homo sapiens	

<400> 29
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<210> 30
<211> 23
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<213> Homo sapiens

<400> 30
gaggtgcagc tggggagtc tgg 23

<210> 31
<211> 23
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<213> Homo sapiens

<400> 31
caggtgcagc tgcaggagtc ggg 23

<210> 32
<211> 23
<212> DNA
<213> Homo sapiens

<400> 32
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35 40 45

Gln Glu Ser Lys Cys His Leu Ile Glu Thr Asn Ile Arg Asp Gln Glu
50 55 60

Glu Leu Lys Gly Lys Lys Val Pro Gln Tyr Pro Cys Leu Trp Val Asn
65 70 75 80

Val Ser Ala Ala Gly Arg Trp Ala Val Leu Tyr His Thr Glu Asp Thr
85 90 95

Arg Asp Gln Asn Gln Gln Cys Ser Tyr Ile Pro Gly Ser Val Asp Asn
100 105 110

Tyr Gln Thr Ala Arg Ala Asp Val Glu Lys Val Arg Ala Lys Phe Gln
115 120 125

Glu Gln Gln Val Phe Tyr Cys Phe Ser Ala Pro Arg Gly Asn Glu Thr

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Leu Phe Trp Pro Thr Phe Leu Leu Thr Gly Gly Leu Leu Ile Ile Ala		
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Thr Ile Gly Thr Leu Thr Lys Asn Asn Asp Thr Met Leu Ser Ala Met		
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Phe Ser Gly Arg Met Glu Val Leu Thr Asp Ser Glu Gly Trp Ile Leu		
50	55	60
Ile Asp Arg Cys Gly Asn His Phe Gly Ile Ile Leu Asn Tyr Leu Arg		
65	70	75
80		
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Leu Ala Glu Ala Lys Tyr Tyr Cys Ile Thr Glu Leu Ala Ile Ser Cys		
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Glu Arg Ala Leu Tyr Ala His Gln Glu Pro Lys Pro Ile Cys Arg Ile		
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Pro Leu Ile Thr Ser Gln Lys Glu Glu Gln Leu Leu Ser Val Ser		
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Phe Asp Lys Leu Ser Leu Arg Phe Asn Glu Arg Ile Leu Phe Ile Lys		
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Asp Arg Lys His Thr Lys Val Glu Phe Pro Glu Ala Arg Ile Tyr Glu
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245 250 255

Glu Leu Met Gln Ala Thr Ser Ser Ala Arg Val Gly Ser Ala Ser Gly
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